

**Table S2.** Putative QS-controlled genes with upstream *lux*-box-like promoter elements.<sup>a</sup>

Motif <sup>b</sup>	Location, strand <sup>b</sup>	Gene number	Gene name	Role	Fold change <sup>c</sup>
<b><u>A</u></b>					
<b>acyatrgth</b>					
accatagta,	-171 to -163, +	Nwi0627	<i>nwiR</i>	putative AHL-	1.3
actatggtc	-212 to -220, -			binding LuxR homolog	
accatggtt,	-266 to -274, -	Nwi0637	<i>coaE</i>	acyl-CoA	1.8
accatggtc	-273 to -265, +			dehydrogenase	
accatggta,	-92 to -100, -	Nwi0914		ABC transporter-	-2.4
accatggtc	-99 to -91, +			related	
accatggtc,	-218 to -226, -	Nwi1316	<i>rpsD</i>	ribosomal protein	-3.1
accatggtt	-225 to -217, +				
accatggtt,	-212 to -220, -	Nwi2653-	<i>nirK</i> ,	potential NO-	2.2 to 19.9
accatggta	-219 to -211, +	2648 <sup>c</sup>	<i>ncgABC</i>	producing/ consuming gene cluster	
<b><u>B</u></b>					
<b>atchdhnddvbgat</b>					

atccgattaatgat,	-104 to -91, +	Nwi0080,		hypothetical	-2.1 to 6.6
atcatcggagtgat,	-15 to -2, +	0402, 0403,			
atcttccaaacgat,	-407 to -420, -	1972, 2908,			
atcctcatggtgat,	-316 to -329, -	3041			
atcattcatccgat	-56 to -69, -				
	-233 to -220, +				
atcagcttggcgat	-67 to -80, -	Nwi0627	<i>nwiR</i>	putative AHL-binding LuxR homolog	1.3
atccgtcaagcgat	-83 to -70, +	Nwi0781		transposase	-4.6
atcaatcgccgat	-52 to -39, +	Nwi1035		UspA, universal stress protein loci	3.0, 3.4
atctttcaacgat	-299 to -312, -	Nwi1286	<i>gcvT</i>	glycine cleavage system	-2.9
atcatccagcgat	-140 to -127, +	Nwi1386	<i>rpsM</i>	ribosomal protein	-3.7
atccgaaagacgat	-127 to -114, +	Nwi2151		Ppx/GppA phosphatase, stringent response	3.2
atcagtatgctgat	-51 to -38, +	Nwi2455		folic acid metabolism	2.6

atctttcagacgat,	-547 to -534, +	2512, 2513	hypothetical	-5.7, -3.8,
atccgataaatgat,	-312 to -299, +		ribosome-	-3.0
atcatttatcgat,	-325 to -312, +		associated	
atctttcagacgat	-77 to -90, -			
atcaaaggaccgat	-443 to -430, +	Nwi2845,	conserved peptidase	3.5
	-246 to -259, -	2846	C14	
atctgcctgaggat	-307 to -294, +	Nwi3028	OmpA/MotB	6.2

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<sup>a</sup>All motifs are also found in the intergenic region between Nwi0627 (*nwiR*) and Nwi0628 (*pgm*). No motifs were detected in the 81 bp intergenic space between Nwi0626 (*nwiI*) and *nwiR*.

<sup>b</sup>Sequences, upstream location, and strand are listed in the order of gene numbers in the gene number column. Some sequence motifs appear on both strands for a single gene or in front of multiple genes.

<sup>c</sup>Fold change is the difference in mRNA transcript levels between AiiA-treated QS-deficient cells and QS-proficient cells ( $P \leq 0.05$ ).

<sup>d</sup>The motif was only found within intergenic region upstream of Nwi2653, the putative start site of the operon.